

SEQUENCE LISTING

<110> Yu, Xuanchuan
Miranda, Maricar
Friddle, Carl Johan

<120> Novel Human Proteases and
Polynucleotides Encoding the Same

<130> LEX-0280-USA

<150> US 60/255,567

<151> 2000-12-14

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1509

<212> DNA

<213> Homo sapiens

<400> 1

atggctcagc	gggtcggtttg	ctgtctggcc	ctgggtggcta	tgtgtctect	agttttccct	60
accgtctcca	gatcgatggg	cccgaggagc	ggggagcctc	aaagggcgctc	gcgaatccct	120
tctcagtcca	gcaaaaggga	acgcgtcgcg	atgaaagagg	cgctgaaagg	tgccatccag	180
attccaacag	tgaacttttag	ctctgagaag	tccaatacta	cagccctggc	tgagttcgga	240
aaatacaatt	ataaagctct	tcctacagtg	gtcagcacca	gctttatcca	gcatgaagtc	300
gtggaagagt	atagccacct	gttcaactatc	caaggctcgg	acccagctt	gcagccctac	360
ctgctgatgg	ctcactttga	tgtggtgcct	gccccgaag	aaggctggga	ggtgccccca	420
ttctctgggt	tgagcgtga	tggtctcatc	tatggtcggg	gcacactgga	cgacaagaac	480
tctgtgatgg	cattactgca	ggccttgagg	ctcctgctga	tcaggaagta	catccccgga	540
agatctttct	tcattttctt	gggccatgat	gaggagtcac	cagggacagg	ggctcagagg	600
atctcagccc	tgctacagtc	aagggcgctc	cagctagctc	tcattgtgga	cgagggggggc	660
ttcatcttgg	atgattttcat	tcctaaacttc	aagaagccca	tcgccttgat	tgcagtctca	720
gagaaggggt	ccatgaacct	catgctgcaa	gtaaacatga	cttcaggcca	ctcttcagct	780
cctccaaagg	agacaagcat	tggtcatcct	gcagctgctg	tcagccgatt	ggagcagaca	840
ccaatgccta	tcataatttg	aagcgggaca	gtggtgactg	tattgcagca	actggcaaat	900
gagtttccct	tcctctgcaa	tataatctgt	agcaaccctc	ggctatttga	accacttata	960
agcaggttta	tgagagaaaa	tcctttaacc	aatgcaataa	tcaggaccac	cacggcactc	1020
accatattca	aagcaggggt	caagtccaat	gtcctcccc	cagtggccca	ggccacagtc	1080
aaacttcgga	ttcaccctgg	acagacagtc	caagaggctc	tagaactcac	gaagaacatt	1140
gtgctgata	acagagtcga	gttccatgtg	ttgagtgcc	ttgaccccc	ccccgtcage	1200
ccttctgagt	acaagggctt	gggctaccag	ctgctccgcc	agaccgtaca	gtccgtcttc	1260
ccggaagtga	atatctactgc	cccagttact	tcctattggca	acacagagac	ccgatttttt	1320
acaaacctca	ccactggcat	ctacaggttc	taccccatct	acatacagcc	tgaagacttc	1380
aaacgcattc	atggagtcga	cgagaaaatc	tcagtcctca	cctatgagag	ccaagtgaac	1440
ttcatcttgg	agttgattca	gaatgctgac	acagaccagg	agccagtttc	tcactctcac	1500
aaactgtga						1509

<210> 2

<211> 502

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Ala Gln Arg Cys Val Cys Val Leu Ala Leu Val Ala Met Leu Leu
 1          5          10          15
Leu Val Phe Pro Thr Val Ser Arg Ser Met Gly Pro Arg Ser Gly Glu
          20          25          30
His Gln Arg Ala Ser Arg Ile Pro Ser Gln Phe Ser Lys Glu Glu Arg
 35          40          45
Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro Thr Val
 50          55          60
Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu Phe Gly
 65          70          75          80
Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser Phe Ile
          85          90          95
Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile Gln Gly
 100          105          110
Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe Asp Val
 115          120          125
Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser Gly Leu
 130          135          140
Glu Arg Asp Gly Val Ile Tyr Gly Arg Gly Thr Leu Asp Asp Lys Asn
 145          150          155          160
Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Ile Arg Lys
          165          170          175
Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp Glu Glu
 180          185          190
Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln Ser Arg
 195          200          205
Gly Val Gln Leu Ala Phe Ile Val Asp Glu Gly Gly Phe Ile Leu Asp
 210          215          220
Asp Phe Ile Pro Asn Phe Lys Lys Pro Ile Ala Leu Ile Ala Val Ser
 225          230          235          240
Glu Lys Gly Ser Met Asn Leu Met Leu Gln Val Asn Met Thr Ser Gly
          245          250          255
His Ser Ser Ala Pro Pro Lys Glu Thr Ser Ile Gly Ile Leu Ala Ala
 260          265          270
Ala Val Ser Arg Leu Glu Gln Thr Pro Met Pro Ile Ile Phe Gly Ser
 275          280          285
Gly Thr Val Val Thr Val Leu Gln Gln Leu Ala Asn Glu Phe Pro Phe
 290          295          300
Pro Val Asn Ile Ile Leu Ser Asn Pro Trp Leu Phe Glu Pro Leu Ile
 305          310          315          320
Ser Arg Phe Met Glu Arg Asn Pro Leu Thr Asn Ala Ile Ile Arg Thr
          325          330          335
Thr Thr Ala Leu Thr Ile Phe Lys Ala Gly Val Lys Phe Asn Val Ile
 340          345          350
Pro Pro Val Ala Gln Ala Thr Val Asn Phe Arg Ile His Pro Gly Gln
 355          360          365
Thr Val Gln Glu Val Leu Glu Leu Thr Lys Asn Ile Val Ala Asp Asn
 370          375          380
Arg Val Gln Phe His Val Leu Ser Ala Phe Asp Pro Leu Pro Val Ser
 385          390          395          400
Pro Ser Asp Asp Lys Ala Leu Gly Tyr Gln Leu Leu Arg Gln Thr Val
          405          410          415
Gln Ser Val Phe Pro Glu Val Asn Ile Thr Ala Pro Val Thr Ser Ile
 420          425          430
Gly Asn Thr Asp Ser Arg Phe Phe Thr Asn Leu Thr Thr Gly Ile Tyr

```

435 440 445
 Arg Phe Tyr Pro Ile Tyr Ile Gln Pro Glu Asp Phe Lys Arg Ile His
 450 455 460
 Gly Val Asn Glu Lys Ile Ser Val Gln Ala Tyr Glu Thr Gln Val Lys
 465 470 475 480
 Phe Ile Phe Glu Leu Ile Gln Asn Ala Asp Thr Asp Gln Glu Pro Val
 485 490 495
 Ser His Leu His His Lys Leu
 500

<210> 3
 <211> 1086
 <212> DNA
 <213> Homo sapiens

<400> 3
 atggctcagc ggtgcgtttg cgtgctggcc ctggtggcta tgctgtctct agttttccct 60
 accgctctcca gatcgatggg cccgaggagc ggggagcadc aaagggcgct gcgaatccct 120
 tctcagttca gcaaagagga acgcgtcgcg atgaaagagg cgctgaaagg tgccatccag 180
 attccacag tgacttttag ctctgagaag tccaatacta cagccctggc tgagttcgga 240
 aaatacattc ataaagtctt tctcacagtg gtcagcacca gctttatcca gcatggaagt 300
 gtggaagagt atagccacct gttcactatc caaggctcgg accccagctt gcagccctac 360
 ctgctgatgg ctcactttga tgtggtgcct gccctgaag aaggctggga ggtgccccca 420
 ttctctgggt tggagcgtga tggcgtcatc tatggtcggg gcacactgga cgacaagaac 480
 tctgtgatgg cattactgca ggccttggag ctctgtctga tcaggaagta catccccga 540
 agatctttct tcattttctt gggccatgat gaggagtcat cagggaacagg ggctcagagg 600
 atctcagccc tgctacagtc aaggggcgtc cagctagcct tcatttggga cgaggggggc 660
 ttcatcttgg atgatttcat tctaaacttc aagaagccca tcgccttgat tgcagtctca 720
 gagaaggggt ccataaacct catgctgcaa gtaaacatga cttcaggcca ccttcagct 780
 cctccaaagg agacaagcat tggcatcctt gcagctgctg tcagccgatt ggagcagaca 840
 ccaatgccta tcataattgg aagcgggaca gtggtgactg tatttcagca actggcaaat 900
 gaggtttatg gagagaaatc ccttaaccaa tgcaataatc aggaccacca cggcactcac 960
 catattcaaa gcagggttca agttcaatgt catccccca gtggccagg ccacagtcaa 1020
 cttccggatt caccctggac agacagtcca agaggtccta gaactcacga agaacttgtt 1080
 ggctga 1086

<210> 4
 <211> 361
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ala Gln Arg Cys Val Leu Ala Leu Val Ala Met Leu Leu
 1 5 10 15
 Leu Val Phe Pro Thr Val Ser Arg Ser Met Gly Pro Arg Ser Gly Glu
 20 25 30
 His Gln Arg Ala Ser Arg Ile Pro Ser Gln Phe Ser Lys Glu Glu Arg
 35 40 45
 Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro Thr Val
 50 55 60
 Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu Phe Gly
 65 70 75 80
 Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser Phe Ile
 85 90 95
 Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile Gln Gly
 100 105 110

Ser	Asp	Pro	Ser	Leu	Gln	Pro	Tyr	Leu	Leu	Met	Ala	His	Phe	Asp	Val
	115						120						125		
Val	Pro	Ala	Pro	Glu	Glu	Gly	Trp	Glu	Val	Pro	Pro	Phe	Ser	Gly	Leu
	130					135						140			
Glu	Arg	Asp	Gly	Val	Ile	Tyr	Gly	Arg	Gly	Thr	Leu	Asp	Asp	Lys	Asn
145				150						155					160
Ser	Val	Met	Ala	Leu	Leu	Gln	Ala	Leu	Glu	Leu	Leu	Leu	Ile	Arg	Lys
		165						170						175	
Tyr	Ile	Pro	Arg	Arg	Ser	Phe	Phe	Ile	Ser	Leu	Gly	His	Asp	Glu	Glu
		180						185					190		
Ser	Ser	Gly	Thr	Gly	Ala	Gln	Arg	Ile	Ser	Ala	Leu	Leu	Gln	Ser	Arg
	195						200						205		
Gly	Val	Gln	Leu	Ala	Phe	Ile	Val	Asp	Glu	Gly	Gly	Phe	Ile	Leu	Asp
	210					215					220				
Asp	Phe	Ile	Pro	Asn	Phe	Lys	Lys	Pro	Ile	Ala	Leu	Ile	Ala	Val	Ser
225				230						235				240	
Glu	Lys	Gly	Ser	Met	Asn	Leu	Met	Leu	Gln	Val	Asn	Met	Thr	Ser	Gly
		245						250						255	
His	Ser	Ser	Ala	Pro	Pro	Lys	Glu	Thr	Ser	Ile	Gly	Ile	Leu	Ala	Ala
		260						265					270		
Ala	Val	Ser	Arg	Leu	Glu	Gln	Thr	Pro	Met	Pro	Ile	Ile	Phe	Gly	Ser
	275					280						285			
Gly	Thr	Val	Val	Thr	Val	Leu	Gln	Gln	Leu	Ala	Asn	Glu	Val	Tyr	Gly
	290					295					300				
Glu	Lys	Ser	Leu	Asn	Gln	Cys	Asn	Asn	Gln	Asp	His	His	Gly	Thr	His
305				310						315				320	
His	Ile	Gln	Ser	Arg	Gly	Gln	Val	Gln	Cys	His	Pro	Pro	Ser	Gly	Pro
		325							330					335	
Gly	His	Ser	Gln	Leu	Pro	Asp	Ser	Pro	Trp	Thr	Asp	Ser	Pro	Arg	Gly
		340						345					350		
Pro	Arg	Thr	His	Glu	Glu	His	Cys	Gly							
	355						360								